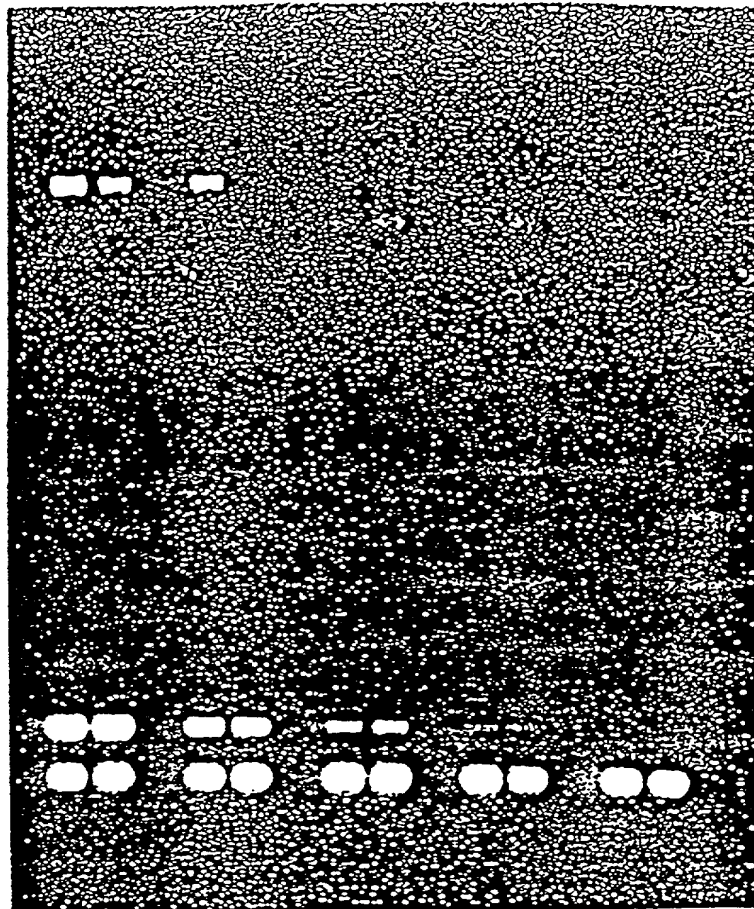


FIG. 2

mouse Bcl-2 →



Actin →

FIG. 3

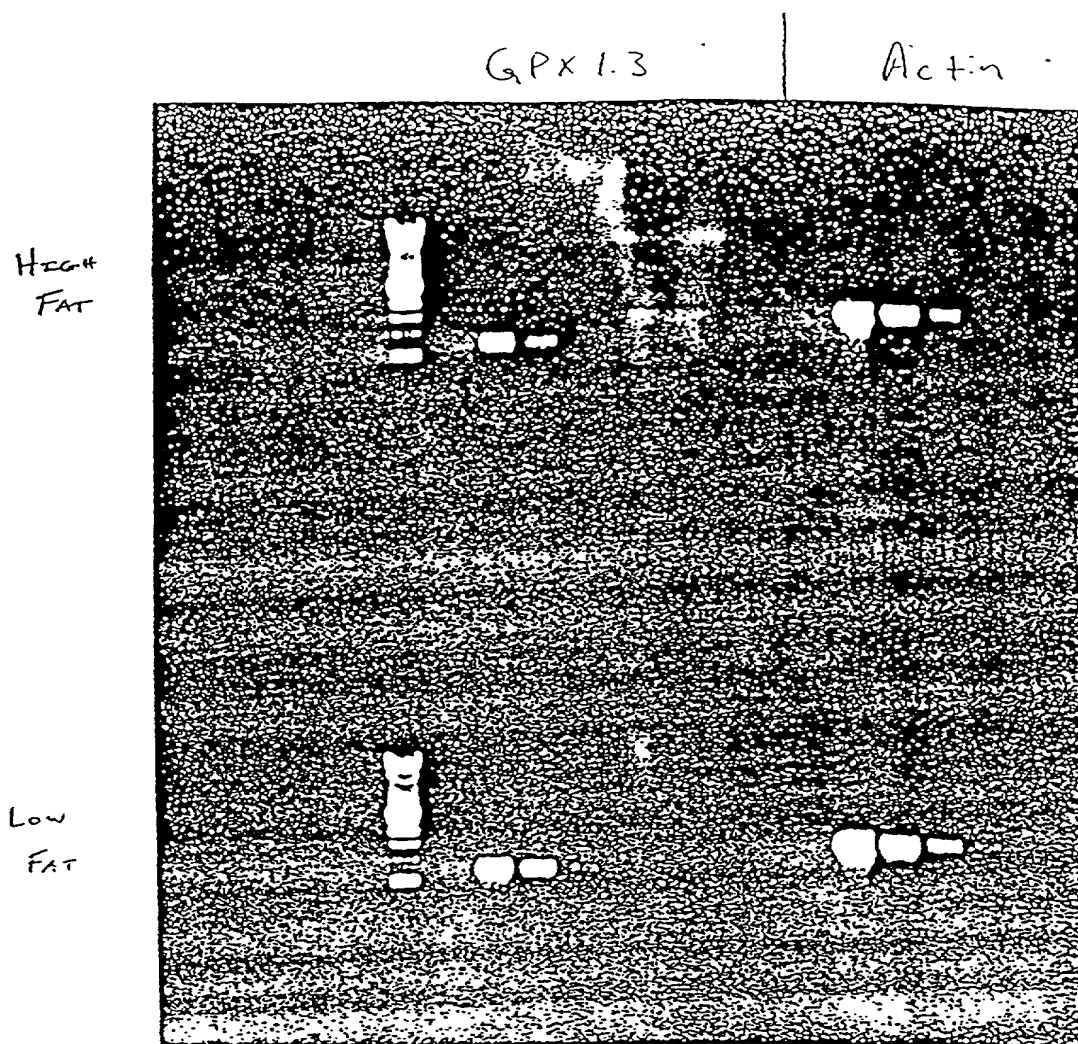


FIG. 4

705007 0280/660

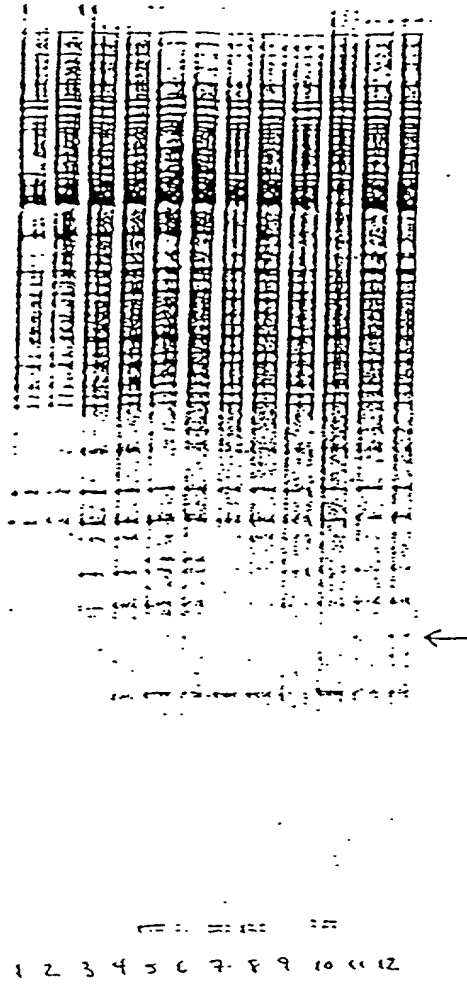


FIG. 5

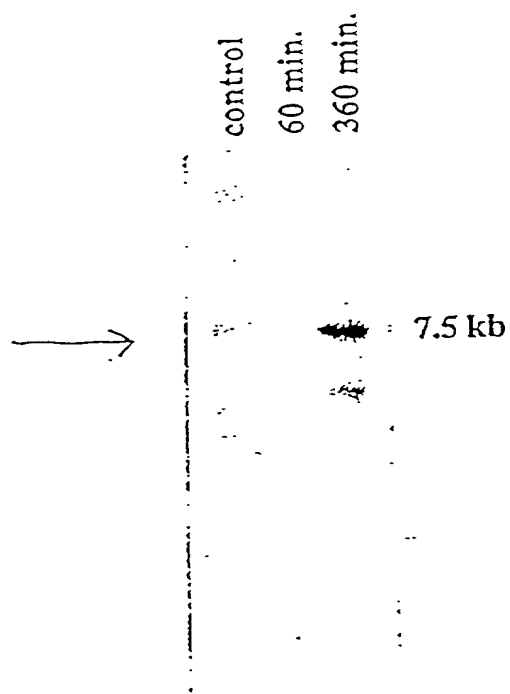


FIG. 6

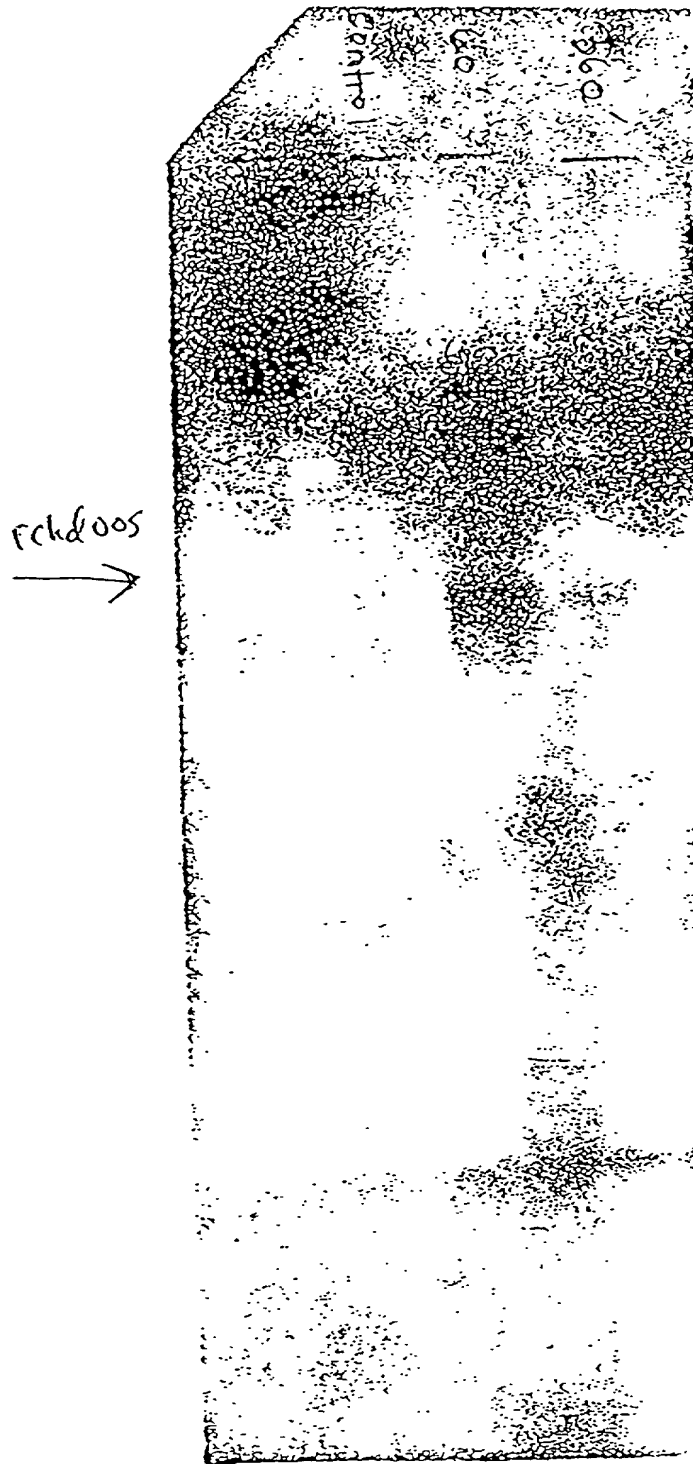


FIG. 7

09970820-100501

10 20 30 40 50 60
 RCHD005.COMPLET(1>288)-> GGCTTAGATGCAGCCTGCAAATTAACTTTTGATTTTTTCATCTTGTGAAAGCAGTCCCTGT
 GGCTTAGATGCAGCCTGCAAATTAACTTTTGATTTTTTCATCTTGTGAAAGCAGTCCCTGT

70 80 90 100 110 120
 RCHD005.COMPLET(1>288)-> TCTATGGCCTAATGAACAACCTCCAGGTAATGAGTATGGTGTGAGGATTTCACCACTA
 TCTATGGCCTAATGAACAACCTCCAGGTAATGAGTATGGTGTGAGGATTTCACCACTA

130 140 150 160 170 180
 RCHD005.COMPLET(1>288)-> ATTCTGCAGGTATATTTTCAGCCACTCTTCTTCAGCATTAGCATCCCTAGTGAGTGCT
 ATTCTGCAGGTATATTTTCAGCCACTCTTCTTCAGCATTAGCATCCCTAGTGAGTGCT

190 200 210 220 230 240
 RCHD005.COMPLET(1>288)-> CCCAAAATATTTTCAGGCTCTATGTAAGGACAACATCTACCCAGCTTTCAGATGTTTGCT
 CCCAAAATATTTTCAGGCTCTATGTAAGGACAACATCTACCCAGCTTTCAGATGTTTGCT

250 260 270 280
 RCHD005.COMPLET(1>288)-> AAAGGTTATGGGAAAAATAATGAACCTCTTCGTGGCTGCATCTAAGCC
 AAAGGTTATGGGAAAAATAATGAACCTCTTCGTGGCTGCATCTAAGCC

FIG. 8

105001 02804660

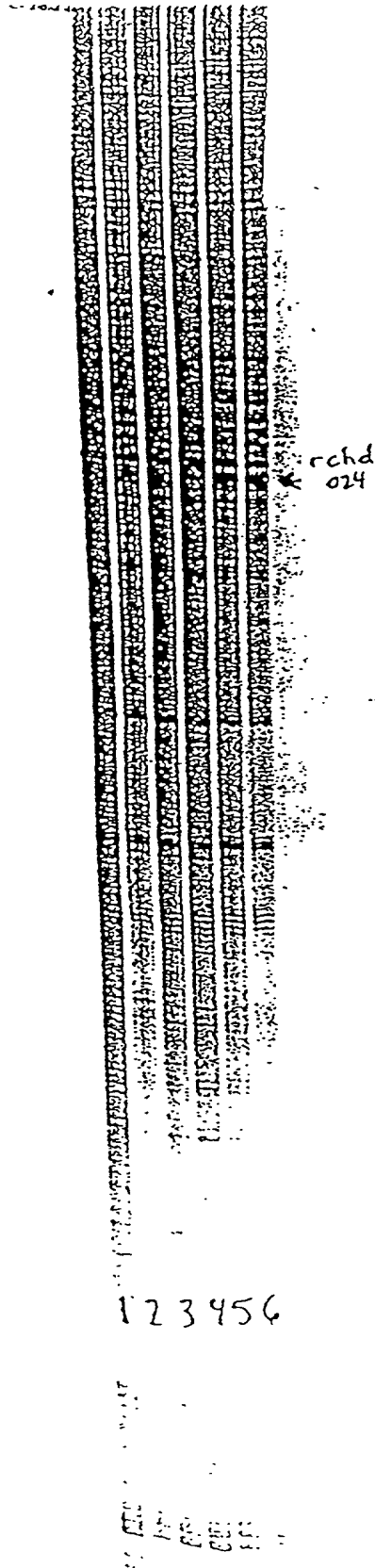
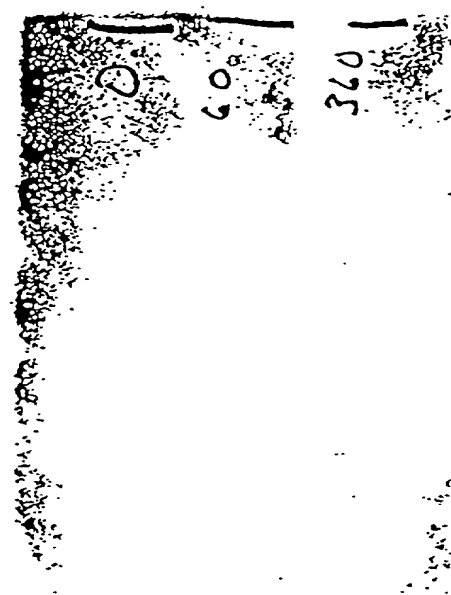


FIG. 9



← rchd 024

FIG. 10

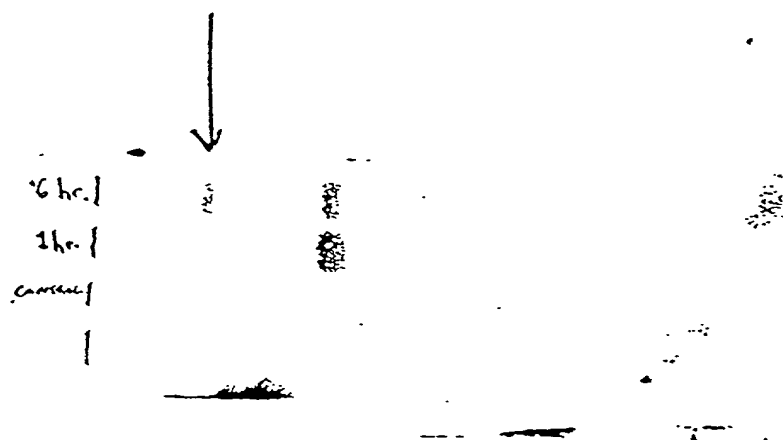


FIG. 11

10 20 30 40 50
RCHD024.COMPLETE.SEQ(1>178)-> AAAAATAAATAAATTAAAGTCTGAGACCAATTTGCCACTGTGAATATAAG
AAAAATAAATAAATTAAAGTCTGAGACCAATTTGCCACTGTGAATATAAG

60 70 80 90 100
RCHD024.COMPLETE.SEQ(1>178)-> CACATTAAACCCAGGAGGAGCCAAGAAGTACACAAACCTCTCTATGAGAA
CACATTAAACCCAGGAGGAGCCAAGAAGTACACAAACCTCTCTATGAGAA

110 120 130 140 150
RCHD024.COMPLETE.SEQ(1>178)-> TTTACCAGTCTTCTTTTCATTTGGCAAGAAAAAGCTCAGGAAAATTTGCTT
TTTACCAGTCTTCTTTTCATTTGGCAAGAAAAAGCTCAGGAAAATTTGCTT

160 170
RCHD024.COMPLETE.SEQ(1>178)-> GTTTAAATTCTATGAGCCTAGTCTATGG
GTTTAAATTCTATGAGCCTAGTCTATGG

FIG. 12

09970830 100501

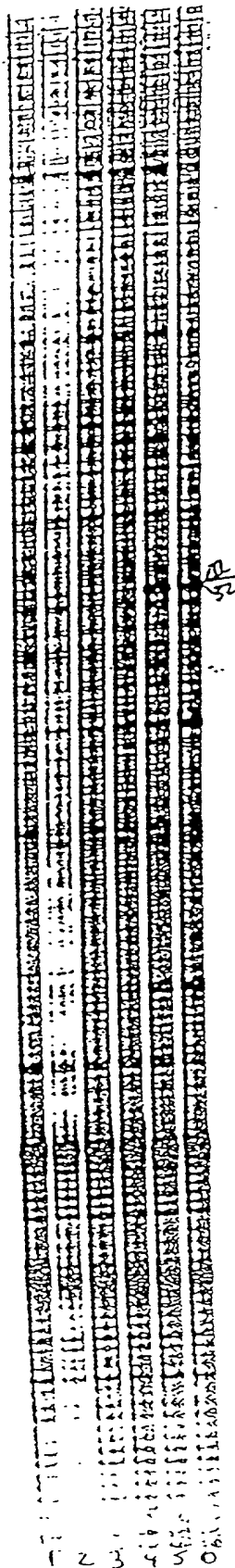


FIG. 13

09970220 10050

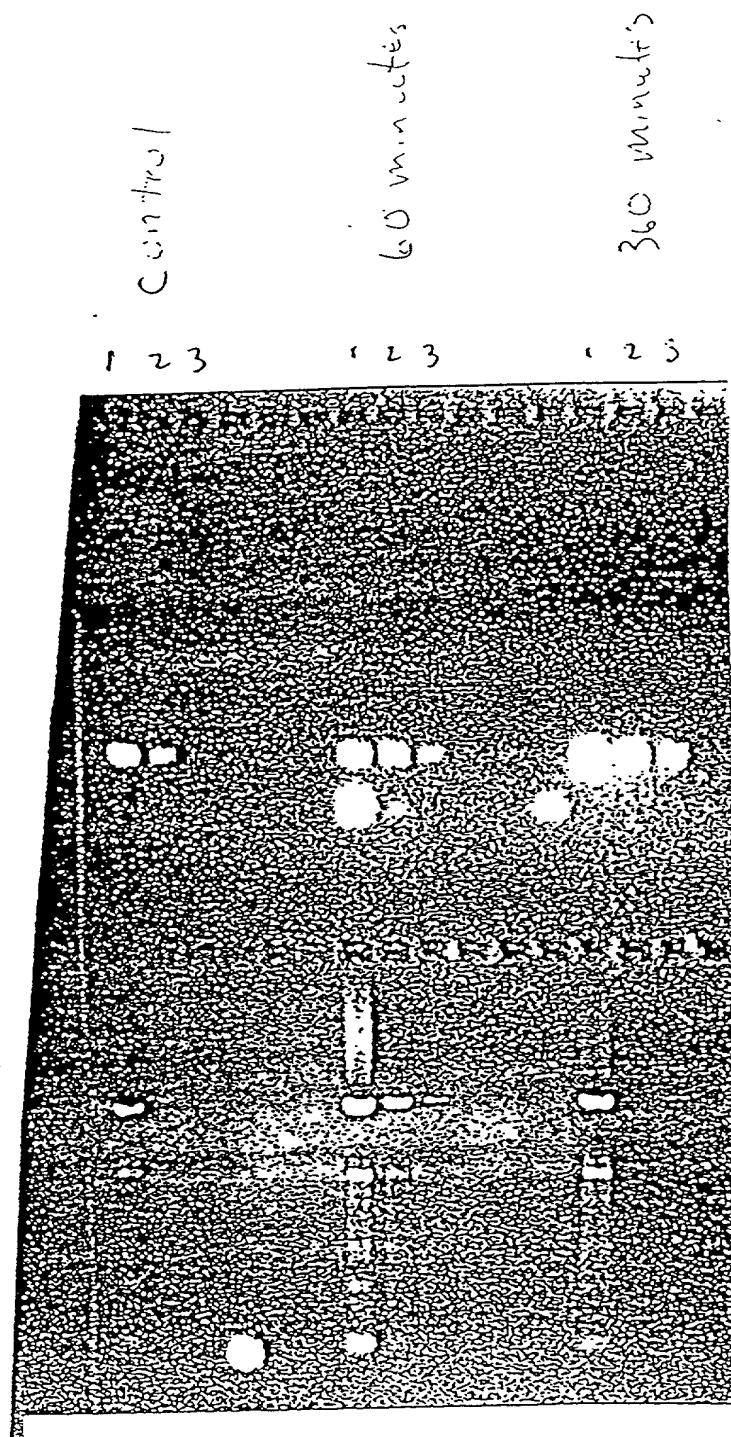


FIG. 14

105001 0330/660

```

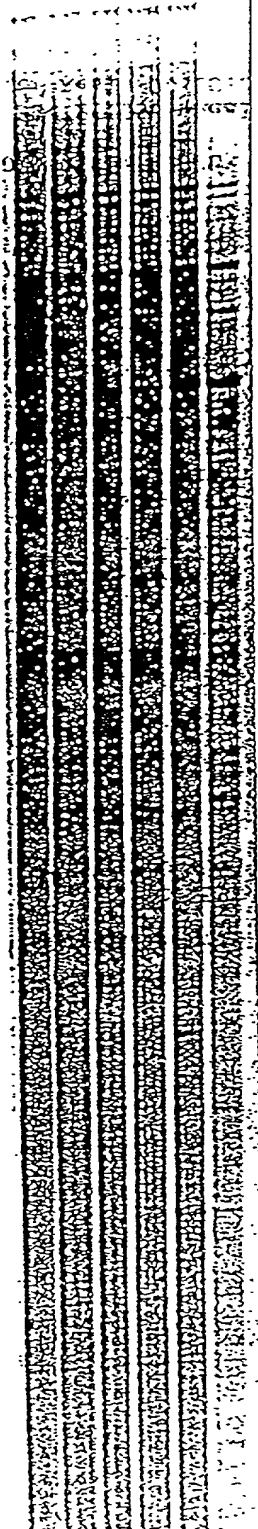
      10      20      30      40      50
RCHD032.COMPLETE.SEQ(1>101)-> GGGTAATTCATTAATTACACTTTAAAATTGGAAAGTGGGATAAGAAATCT
      GGGTAATTCATTAATTACACTTTAAAATTGGAAAGTGGGATAAGAAATCT

      60      70      80      90     100
RCHD032.COMPLETE.SEQ(1>101)-> AAAGTAAACCAGCTTATCTTTGAAACAATATTATTTTGAAATTGGCTTTA
      AAAGTAAACCAGCTTATCTTTGAAACAATATTATTTTGAAATTGGCTTTA

RCHD032.COMPLETE.SEQ(1>101)-> A
      A
  
```

FIG. 15

1 2 3 4 5 6



← rchd 036

FIG. 16

09970820 409504
T0500T 0280/660



rchd 036

FIG. 17

09970830 005001

RCHD036.COMPLETE.SEQ(1>184)-> GGCTTGGTGGTGATGCCTACAAGAAATGTTTACATACAAACACTCTATAC
 GGCTTGGTGGTGATGCCTACAAGAAATGTTTACATACAAACACTCTATAC

RCHD036.COMPLETE.SEQ(1>184)-> ATCTAACTCCCGAAAAAGGACCAGCTATTTTCGGCAACAGAAAAAGACAA
 ATCTAACTCCCGAAAAAGGACCAGCTATTTTCGGCAACAGAAAAAGACAA

RCHD036.COMPLETE.SEQ(1>184)-> GCATTTTCAGAGGAGCGTTGCTTTTCCTTAAAGACCTAACTCACTTAAGTCT
 GCATTTTCAGAGGAGCGTTGCTTTTCCTTAAAGACCTAACTCACTTAAGTCT

RCHD036.COMPLETE.SEQ(1>184)-> TACAAACAGAAATAACAAGGAGGACAATTTTCTA
 TACAAACAGAAATAACAAGGAGGACAATTTTCTA

FIG. 18

105007 02802650

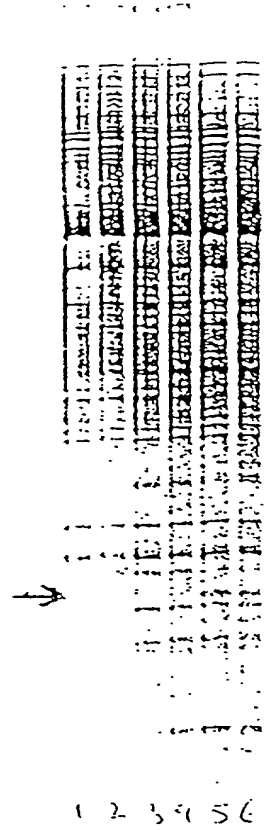


FIG. 19

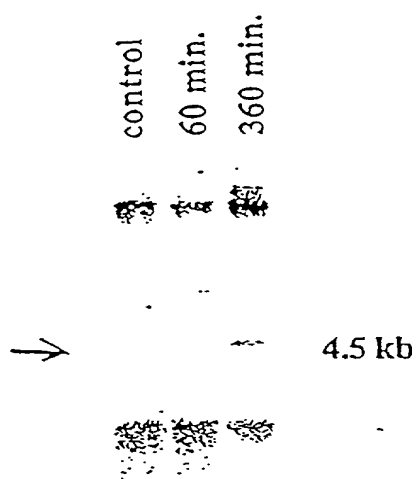


FIG. 20

105001 02304660

1 2 3

57 61 77

←

208

FIG. 21

10 20 30 40 50 60
 RCHD502K. COMPLETE (1>284)-> CTTGGGGATGCTGTTGGAGGAATCCTCATGAAGCGCTTTGTTTCTCTCTACAAGCCAT
 CTTGGGGATGCTGTTGGAGGAATCCTCATGAAGCGCTTTGTTTCTCTCTACAAGCCAT

70 80 90 100 110 120
 RCHD502K. COMPLETE (1>284)-> TCCCCGCATAGCTAACCACATCATCACCATCTCCATGATCCTTTGTTCTCCTTTGTTCTT
 TCCCCGCATAGCTAACCACATCATCACCATCTCCATGATCCTTTGTTCTCCTTTGTTCTT

130 140 150 160 170 180
 RCHD502K. COMPLETE (1>284)-> CATGGGATGCTCCACCCCAACTGTGGCCGAAGTCTACCCCCCTAGCACATCAAGTTCTAT
 CATGGGATGCTCCACCCCAACTGTGGCCGAAGTCTACCCCCCTAGCACATCAAGTTCTAT

190 200 210 220 230
 RCHD502K. COMPLETE (1>284)-> ACATCCGCAGTCTCCTGCCTGCCGCAGGGACTGCTCGTGCCCAGATTCTATCTTCCACCC
 ACATCCGCAGTCTCCTGCCTGCCGCAGGGACTGCTCGTGCCCAGATTCTATCTTCCACCC

250 260 270 280
 RCHD502K. COMPLETE (1>284)-> GGTCTGTGGAGACAATGGAATCGAGTACCTCTCCCCCTTGCCATG
 GGTCTGTGGAGACAATGGAATCGAGTACCTCTCCCCCTTGCCATG

FIG. 22

[illegible]

1 2 3 4 5 6

FIG. 23

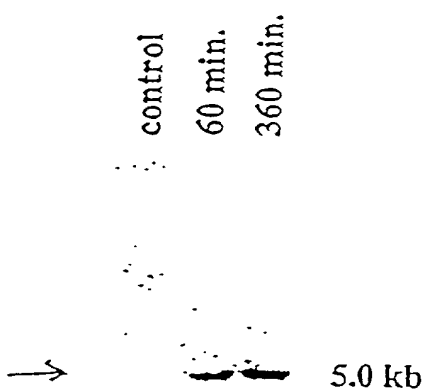


FIG. 24



FIG. 25

09970220 005005 02807660

rchd 523 →

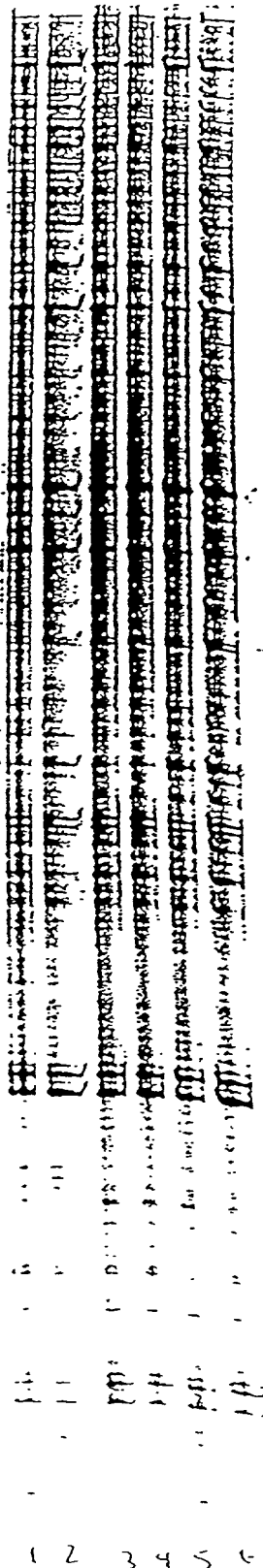


FIG. 26

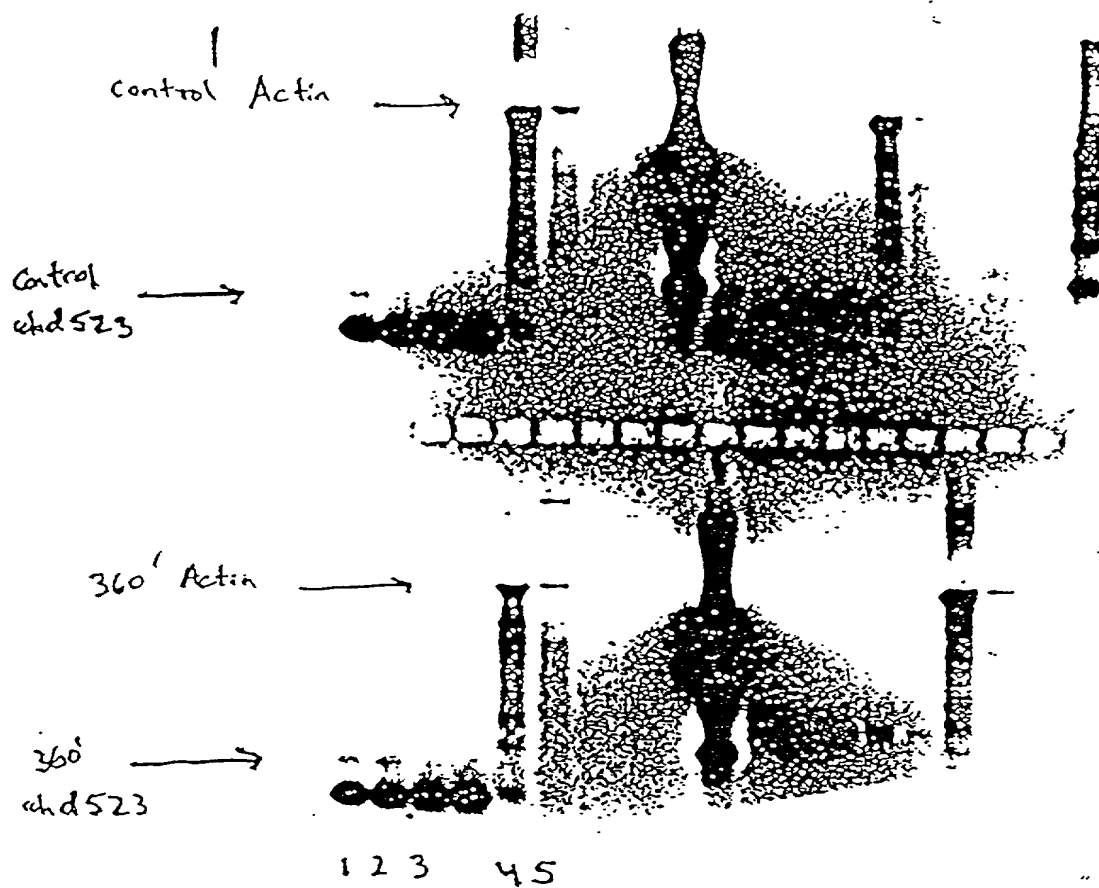


FIG. 27

fchd523

GGCTTACCATOGATGCGGCGGGGATCCAGGGCTCAGAGGGAGGACGCAACCGCCAGCCAG	61
COGGGAACCTTCCCTGCGGGGCTCCAGGGCGGGTCTCTTCTCTCTAGCCCTGCTCAGGCATTCGGCAGGTCCAGC	140
AGAGGTACACCTCTCTGAGCGGGTTCCAAGTGCACTCCAGGCTGATGGACCTGACCAAGGAGGCTTCCAGGAGCACAG	219
AAGGGGCTGCAACCCAGGTACCCAGAGAGTGAGCAGCTCCAGCGGGACTGTGCACGGTGGCCGACACCCGACAGGGACG	298
CCACCGGAGCAGCAGCGGGAGGGGCCCTGGCTCCAGGATGCAACATGCGGGTGTGAGGAGCATCTGTCTTCCCACT	377
CTCTGCAGTTAACAACCCAAACCCAAACCAACCAAGGTGCTCTCTCTGGGGAGTTTCTCTGTCTGACAAATGCCAGGCTC	456
ACTTCAAGGAGAATCAAGCTTCTTTCTAAAGATGGATTACCAATTTAAACAGAGCTCTGGGAGCCTTTGGCAAATCT	535
M D V T S Q A R G V G L E M	14
TGAAAGCTGCAAGGGCAGAGAC ATG GAT GTG ACT TCC CAA GCC CGG GGC GTA GGC CTG GAG ATG	600
Y P G T A Q P A A P N T T S P E L N L S	34
TAC OCA GGC ACC GCG CAG OCT GCG GCC CCC AAC ACC ACC TCC CCC GAG CTC AAC CTG TCC	664
H P L L G T A L A N G T G E L S E H Q Q	54
CAC CCG CTC CTG GGC ACC GGC CTG GGC AAT GGG ACA GGT GAG CTC TCG GAG CAC CAG CAA	724
Y V I G L F L S C L Y T I F L F P I G F	74
TAC GTG ATC GGC CTG TTC CTC TCG TGC CTC TAC ACC ATC TTC CTC TTC CCC ATC GGC TTT	780
V G N I L I L V V N I S F R E K M T I P	94
GTG GGC AAC ATC CTG ATC CTG GTG AAC ATC AGC TTC CGC GAG AAG ATG ACC ATC CCC	840
D L Y F I N L A V A D L I L V A D S L I	114
GAC CTG TAC TTC ATC AAC CTG GCG GTG GCG GAC CTC ATC CTG GTG GCC GAC TCC CTC ATT	900
E V F N L H E R Y Y D I A V L C T F M S	134
GAG GTG TTC AAC CTG CAC GAG CGG TAC TAC GAC ATC GCC GTC CTG TGC ACC TTC ATG TCG	960
L F L R V N M Y S S V F F L T W M S F D	154
CTC TTC CTG CGG GTC AAC ATG TAC AGC AGC GTC TTC TTC CTC ACC TGG ATG AGC TTC GAC	1020
R Y I A L A R A M R C S L F R T K H H A	174
CGC TAC ATC GCC CTG GCC AGG GCC ATG CGC TGC AGC CTG TTC CGC ACC AAG CAC CAC GCC	1080
R L S C G L I W M A S V S A T L V P F T	194
CGG CTG AGC TGT GGC CTC ATC TGG ATG GCA TCC GTG TCA GCC ACG CTG GTG CCC TTC ACC	1140
A V H L Q H T D E A C F C F A D V R E V	214
GCC GTG CAC CTG CAG CAC ACC GAC GAG GCC TGC TTC TGT TTC GCG GAT GTC CGG GAG GTG	1200
Q W L E V T L G F I V P F A I I G L C Y	234
CAG TGG CTC GAG GTC ACG CTG GGC TTC ATC GTG CCC TTC GCC ATC ATC GGC CTG TGC TAC	1260
S L I V R V L V R A H R H R G L R P R R	254
TCC CTC ATT GTC CGG GTG CTG GTC AGG GCG CAC CGG CAC CGT GGG CTG CGG CCC CGG CGG	1320
Q K A L R M I L A V V L V F F V C W L P	274
CAG AAG GCG CTC CGC ATG ATC CTC GCA GTG GTG CTG GTC TTC TTC GTC TGC TGG CTG CGG	1380
E N V F I S V H L L Q R T Q P G A A P C	294
GAG AAC GTC TTC ATC AGC GTG CAC CTC CTG CAG CGG ACG CAG CCT GGG GCC GCT OCT TGC	1440
K Q S F R H A H P L T G H I V N L A A F	314
AAG CAG TCT TTC CGC CAT GCC CAC CCC CTC ACG GGC CAC ATT GTC AAC CTC GCC GCC TTC	1500

FIG. 28A

T0500T" 02802650

S N S C L N P L I Y S F L G E T F R D K 334
 TCC AAC AGC TGC CTA AAC CCC CTC ATC TAC AGC TTT CTC GGG GAG ACC TTC AGG GAC AAG 1560
 L R L Y I E Q K T N L P A L D R F C H A 354
 CTG AGG CTG TAC ATT GAG CAG AAA ACA AAT TTG CCG GCC CTG GAC CGC TTC TGT CAC GCT 1620
 A L K A V I P D S T E Q S D V R F S S A 374
 GCC CTG AAG GCC GTC ATT CCA GAC AGC ACC GAG CAG TGG GAT GTG AGG TTC AGC AGT GCC 1680
 V * 375
 GTG TAG ACAGCCTTGGCCCATAGGCCAGCCAGGGTGTGACTGGGAGCTGCACACACTGGGTGGACACAAGGCA 1757
 CGGCCAGTTCATGTCTCTAAACTGGGTCAGATGTGGCTTCTGGCTCTGGGGCTGGGGAGGGTCACGGCTTGGCTGGT 1836
 CAACCTGGGGCTGCTTAGGAAACCTCAGGACTGGTCACTTGCACCTCTCACACAGAATGCTACAATCCCAAGGGCT 1915
 CGCCCCGAGGGTCCAAAGGGCAGGGTGAACAGGCTGTCAACCCAGCTCTCCCGGCCAAACCTGGCTGGCGCTGCACC 1994
 TCCCGCTGCTGCAGGAAACATTTCTGACACCGTGGACAGGAAAGCCACAGGAGAGGCCACTGTGGGTGAAGCCGCT 2073
 CAGTTACACAGGAACCTAAAGCAATCTGCCACCGTGGGGGAACGTAGCGCTGGAGATGCAAGGTGCTGGTGGGTCTGA 2152
 GCTGGAGGTGGGGTGTGTCTCTGTGCCACGGTCTGAGCTAGCTAGCGCACCGCCGAGTTAAAGAGGAGAAGGAAAA 2231
 CATGCTGCTCTGGTGCAGGCTGAGCGTCTCCATCTTCCAGGATGGCAGCAATGGCGCTGTGCGGCTCACCGAGCCC 2310
 AGGAGGAGCAGCAGCGCTCGGGCCGGAGCAGCAGGAAGGCCCTCTGTGGAGGCGCCGCGCTCTGCTCGGGGTGGTTC 2389
 AGTCACTGCTTGTGACATCAACATGGCAATGCACTCATGTGACTGGGACCGTGGGAGCTGGCGTGTGGGTAGTGG 2468
 GGTGCCAGGACAATGAAATACTCCAGCACTGTGGCTGAAGAAATTGGTTTCTACAGAAGTAACAGCTGGGGACAACCTGC 2547
 GATGATGATGTAAAAACCTTCCATAAAATAAGCC 2582

FIG. 28B

105001" 0280/660

rchd 528 →

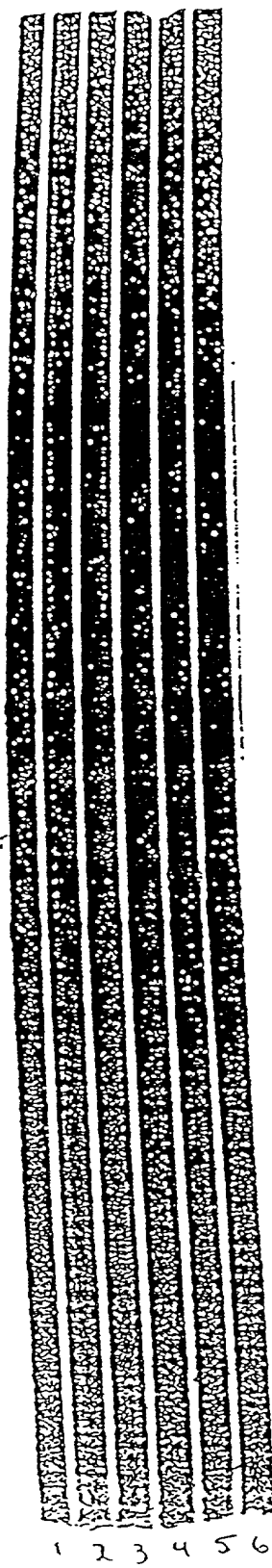


FIG. 29

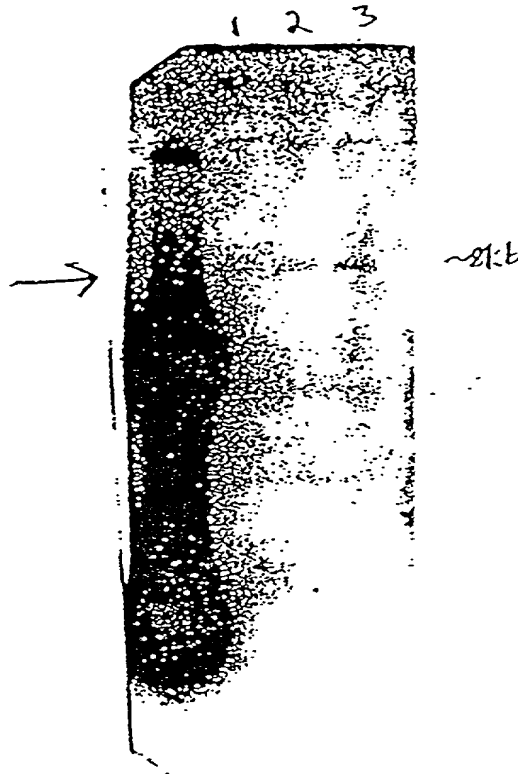


FIG. 30

105001 " 02802660

```

      10      20      30      40      50
RCHD528.COMPLETE.SEQ(1>128)-> GGGAGGTGGGCTCCTGCTCATCCTAGGCATCGCACTGATTGTTACCTGTT
      GGGAGGTGGGCTCCTGCTCATCCTAGGCATCGCACTGATTGTTACCTGTT

      60      70      80      90     100
RCHD528.COMPLETE.SEQ(1>128)-> GCAGAAAGAATAAAAAATGACATAAGCAAACATCTTCAAAAGTGGAGAT
      GCAGAAAGAATAAAAAATGACATAAGCAAACATCTTCAAAAGTGGAGAT

      110     120
RCHD528.COMPLETE.SEQ(1>128)-> TTCCAAATGTCCCCGTATGCTGAATACC
      TTCCAAATGTCCCCGTATGCTGAATACC
```

FIG. 31

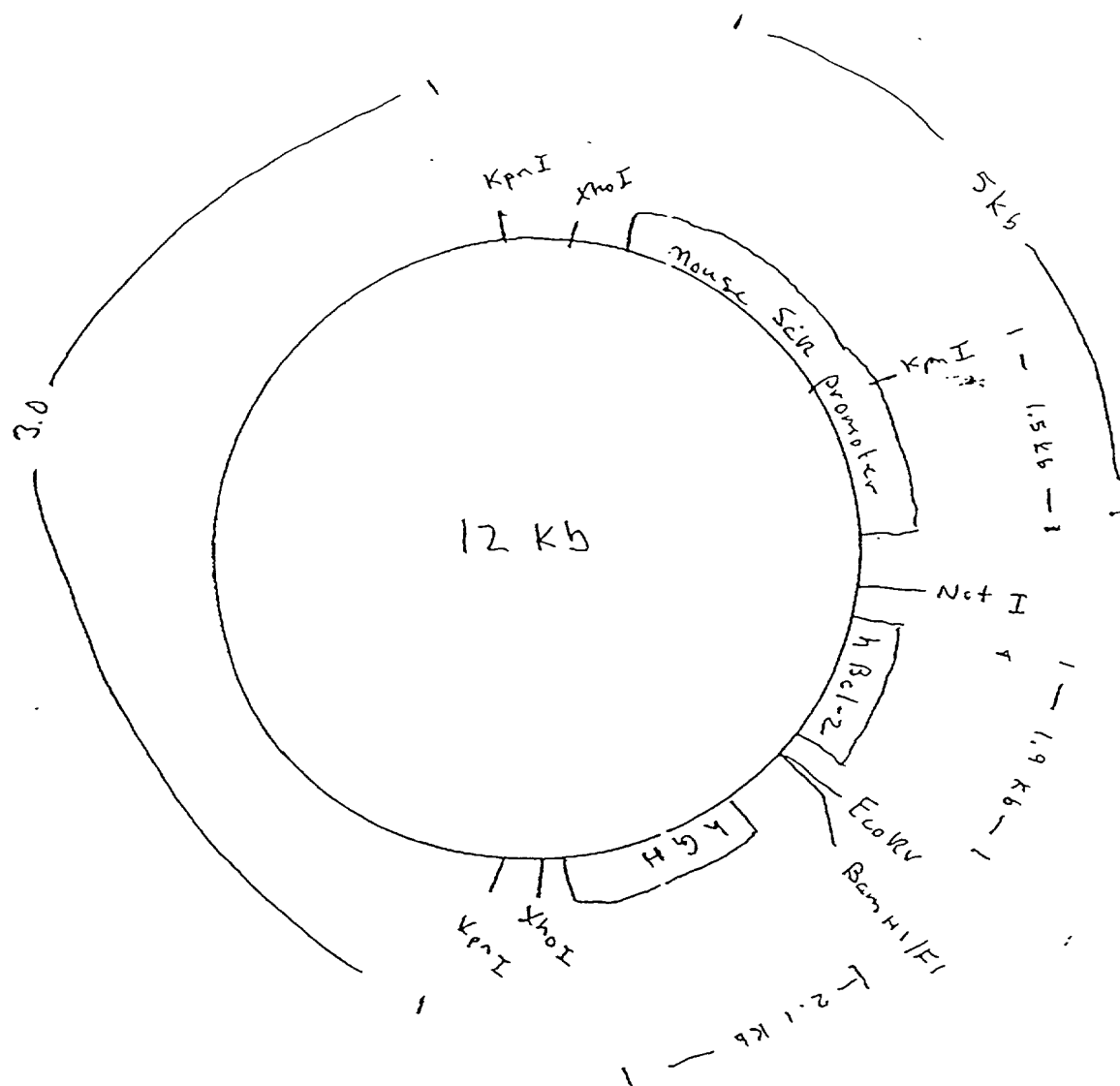
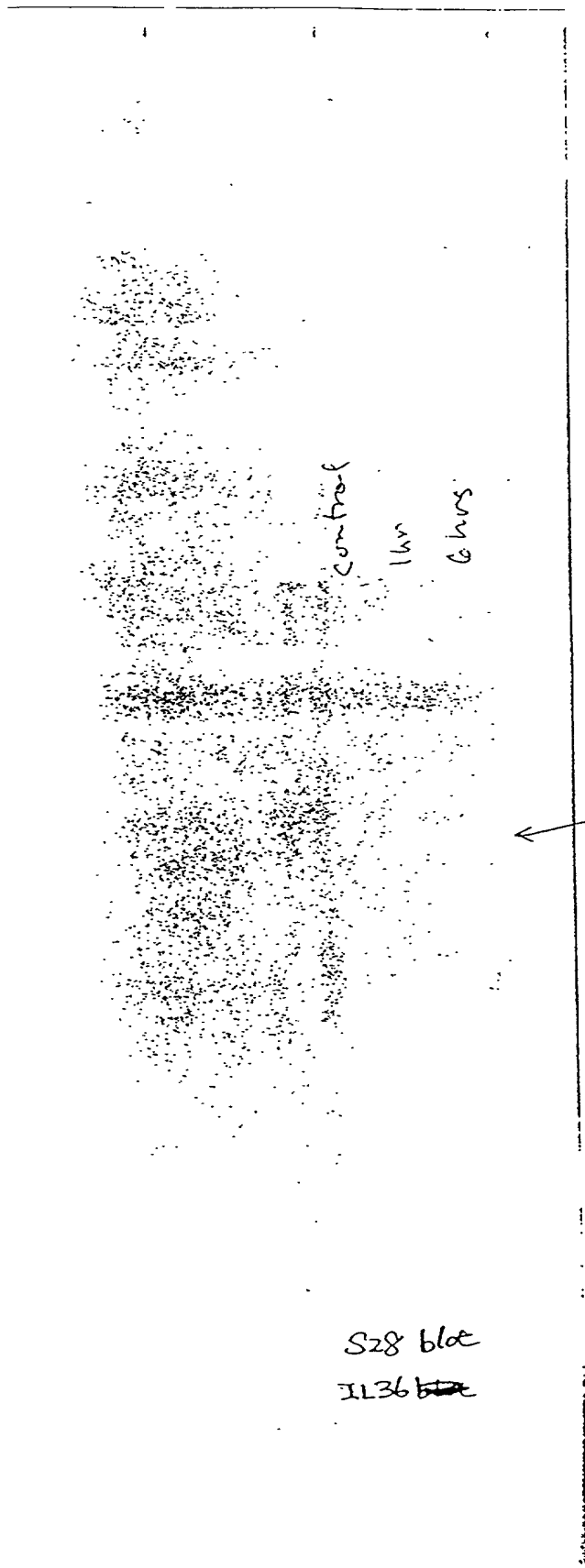


FIG. 32

105001 02802650



control

1hr

6hrs

S28 blot

IL36 blot

FIG. 33

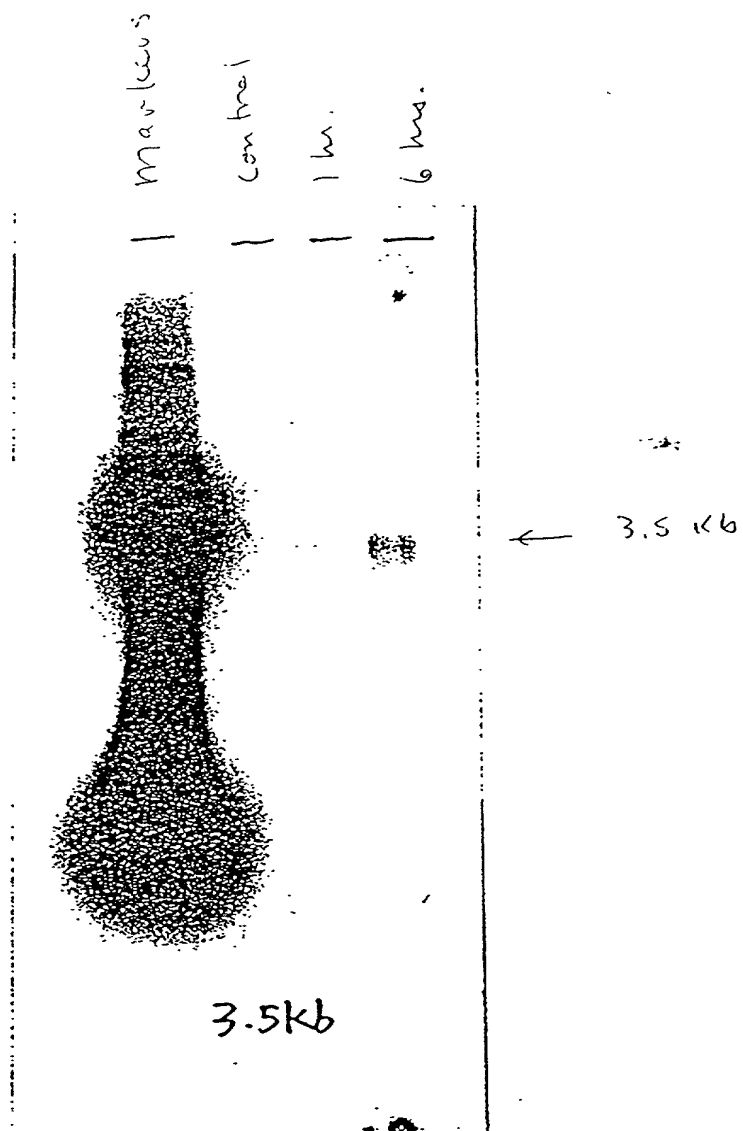


FIG. 34

FCHD534

GAATTCGGCACGAGGMCAGGAGCTCCTTTWCTGGCTCTCCATCATGGGGCTTAGGGTTGAGTCTTCA 68
 GGTTCCTGGGGGAGGAAGGACGGGCACTCAGGAGGCCCCCTCCCATCCACAGCCCCCTTTTGGGAGGGGGAAACTTG 147
 GCAACCCCGGAGGCATGTGGATCTTTTCTAAGCAAGATGCTGAGCTGGAAAGATGGGGGTGTAAGGTAATGTCCAAA 226
 CTGAAACTTTGCCAGGCACTGGGAGAGGCTGTGAACCTCTTTCTGGCTTTAGAATTTAGGTCTAGATCCAAAAGGCTA 305
 AGTACCCCTTGGGGGCTAACAGAGGCATGCTGGGCTGAGCTGAACCTTCTGGTGCACCTGGCCCCCTGGCTGACTGCTC 384
 TTCTGCAGGAAGTTGGAGGAGATTCTGAAGTTGATTCTCAGGCTGATGTCCAAGGGGTTGGAGTTTCTGATGTCT 463
 TTCTGCTCTCCCTCTCTTTTCTTTCTCTCCCTACCAGGTCCACTTCTTTCAGAGGGGCTGGGTGCTCTAAAAGTTCTC 542
 CTGTTAAAGTTTAGAGCAAATTTGGTTATTATTTTAAATCAATAAACTTTTAAAGTACTAAGACAACCTTCTAAGAGG 621
 GGAGTGGACAGAGGGGCTGGTGGCAGCTCACAGTTTCTTTCTGACCTTTGGTCTCACCCACCAAGTGTCCCACTGAG 700
 TGCCCCACTTGGCCACTGAGGTAATGCTGGGCTCCACAGTCCAGATCCACAGGGGCGAGCCATGTGGGAGTGGC 779
 GGCTGATTGTTACCCAGTAGTGTGATAGCACATTATTCATAACAGCCAAAGAGAGGAAGCAACCCAAATGTCCATTAG 858
 CTGATAAATGGATAAATGAAATATGGTAACTGGAAGATGAATATCATTCACCCATGAAAAAGAAAGGAAGTCCAGCA 937
 CCAAAAGTGTCTACACATGGATGAACCTTGGTGGTCCATGAAAGAAGAGCCACCAAAAGGCCATAT 1016
 M S R M G K P I E T Q K S P P P 16
 ATTGTATGAAATGAA ATG TCC AGA ATG GGC AAA CCC ATA GAG ACA CAA AAA TCT CCG CCA CCT 1079
 P Y S R L S P R D E Y K P L D L S D S T 36
 CCC TAC TCT CCG CTG TCT OCT CCG GAC GAG TAC AAG CCA CTG GAT CTG TCC GAT TCC ACA 1139
 L S Y T E T E A T N S L I T A P G E F S 56
 TTG TCT TAC ACT GAA ACG GAG GCT ACC AAC TCC CTC ATC ACT GCT CCG GGT GAA TTC TCA 1199
 D A S M S P D A T K P S H W C S V A Y W 76
 GAC GCC AGC ATG TCT CCG GAC GCC ACC AAG CCG AGC CAC TGG TGC AGC GTG GCG TAC TGG 1259
 E H R T R V G R L Y A V Y D Q A V S I F 96
 GAG CAC CCG ACG CCG GTG GGC CCG CTC TAT GCG GTG TAC GAC CAG GCC GTC AGC ATC TTC 1319
 Y D L P Q G S G F C L G Q L N L E Q R S 116
 TAC GAC CTA CCT CAG GGC AGC GGC TTC TGC CTG GGC CAG CTC AAC CTG GAG CAG CCG AGC 1379
 E S V R R T R S K I G F G I L L S K E P 136
 GAG TCG GTG CCG CGA ACG CCG AGC AAG ATC GGC TTC GGC ATC CTG CTC AGC AAG GAG CCC 1439
 D G V W A Y N R G E H P I F V N S P T L 156
 GAC GGC GTG TGG GCC TAC AAC CCG GGC GAG CAC CCC ATC TTC GTC AAC TCC CCG ACG CTG 1499
 D A P G G R A L V V R K V P P G Y S I K 176
 GAC GCG CCC GGC GGC CCG GCC CTG GTC GTG GGC AAG GTG CCC CCC GGC TAC TCC ATC AAG 1559
 V F D F E R S G L Q H A P E P D A A D G 196
 GTG TTC GAC TTC GAG CCG TCG GGC CTG CAG CAC GCG CCC GAG CCC GAC GCC GCC GAC GGC 1619
 P Y D P N S V R I S F A K G W G P C Y S 216
 CCC TAC GAC CCC AAC AGC GTC CCG ATC AGC TTC GCC AAG GGC TGG GGC CCC TGC TAC TCC 1679
 R Q F I T S C P C W L E I L L N N P R * 235
 CCG CAG TTC ATC ACC TCC TGC CCC TGC TGG CTG GAG ATC CTC CTC AAC AAC CCC AGA TAG 1739

FIG. 35A

TGGCGGCCCCGGGGGAGGGGGGGTGGGAGGCCCCGGCCACGCCACCTGCGGGCTCGAGAGGGGGCGATGCCCAGA 1818
 GACACAGCCCCCAGGACAAAACCCCCAGATATCATCTACCTAGATTTAATATAAAGTTTTATATATTATATGGAAAT 1897
 ATATATTATACTTGTAAATATGGAGTCATTTTACAATGTAATTATTTATGTATGGTCAATGTGTATATGGACAAA 1976
 ACAAGAAAGACGCACTTTGGCTTATAATTCTTTCAATACAGATATATTTCTTTCTCTCTCTCTCTCTCTCTTACT 2055
 TTTTATATATATATAAAGAAAATGATACAGCAGAGCTAGGTGGAAGAGCTGGGTTTGGTGTATGGTTTITGAGATA 2134
 TTAATGCCAGACAAAAAGCTAATACCAGTCACCTGATAATAAAGTATTCGCATTATAGTTTTTTTTAAACTGTCTTCT 2213
 TTTTACAAAGAGGGGGCAGGTAGGGCTTCAGCGGATTCTGACCCATCATGTACCTTGAAACTTGACCTCAGTTTTCAG 2292
 TTTTACTTTTATTGGATAAAGACAGAACAAATTGAAAAGGGAGGAAAGTCACATTTACTCTTAAGTAAACAGAGAAAG 2371
 TTCTGTGTGTCTCTCTCTGCCATGGCTATGGGGTGTCCAGTGGATAGGGATGGCGGTGGGGAAAGGAGAATACACTGG 2450
 CCATTTATCTCGACAAAGCTCTTCAGTCTGATGGAAGAGGTTTCATGCCCTAGCCTAGAAAGGCCAGGTCCATGACCC 2529
 CCATCTTTGAGTTATGAGCAAGCTAAAAGAAGACACTATTTCTCACCATTTTGTGGAATGGCCTGGGGAACAAAGACT 2608
 GAAATGGGCTTGAGCCCACTGCTACCTTGACAGAAACCATCTGAGCCCCGTAGATCTTTTATGACCTCCACAGGC 2687
 TATTTCCACCCCCAGCCAAAAATAGCTCAGAACTGCCCATCCAGGGCTGTATTAAATGATTTATGTAAAGGCAGATG 2766
 GTTTATTTCTACTTTGTAAAAGGGAAAAGTTGAGGTTCTGGAAGGATAAATGATTTGCTCATGAGACAAAATCAAGGTT 2845
 AGAAGTTACATGGAATGTAGGACCAGAGCCATATCATTAGATCAGCTTTCTGAAGATATTTCTCAAAAAAGAAAGTC 2924
 TCCTTGCCAGATAACTAAGAGGAATGTTTCATTGTATATCTTTTTTCTTGGAGATTATATTAACATATTAAAGTGCTC 3003
 TGAGAAGTCTGTGTATTATCTCTTGCTGCATAATAAATTATCCCAAACTTAAAAAAAAAAAAAAAAAAAAAACTCGA 3082
 G 3083

FIG. 35B